

1/20

## SEQUENCE LISTING

&lt;110&gt; INSTITUT NATIONAL DE LA RECHERCHE AGRONOMIQUE

MILAN, Denis

ANDERSSON, Leif

LOOFT, Christian

ROBIC, Annie

ROGEL-GAILLARD, Claire

IANNUCCELLI, Nathalie

GELLIN, Joël

KALM, Ernst

LE ROY, Pascale

CHARDON, Patrick

<120> VARIANTS OF THE GAMMA CHAIN OF AMPK, DNA SEQUENCES ENCODING  
THE SAME, AND USES THEREOF

&lt;130&gt; MJPCb539-99

&lt;140&gt;

&lt;141&gt;

&lt;150&gt; EP 99402236.3

&lt;151&gt; 1999-09-10

&lt;150&gt; EP 00401388.4

&gt;151&gt; 2000-05-18

&lt;160&gt; 32

&lt;210&gt; 1

&lt;211&gt; 1867

&lt;212&gt; DNA

&lt;213&gt; Sus scrofa

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (472) .. (1389)

&lt;400&gt; 1

ttcctagagc aaggagagag ccgttcatgg ccatcccgag ctgtaaccac cagctcagaa 60

agaagccatg gggaccaggg gaacaaggcc tctagatgga caaggcagga ggatgtagag 120

gaaggggggc ctccggggccc gaggggaaggt ccccgagcca ggccagttgc tgagtccacc 180

gggcaggagg ccacattccc caaggccaca cccttgggccc aagccgctcc cttggccgag 240

gtggacaacc cccaacaga gcgggacatc ctcccctctg actgtgcagc ctcagcctcc 300

gactccaaca cagaccatct ggatctgggc atagagttct cagcctcggc ggcgtcgggg 360

gatgagcttg ggctggtgga agagaagcca gccccgtgcc catccccaga ggtgctgtta 420

cccaggctgg gctgggatga tgagctgcag aagccggggg cccagggtcta c atg cac 477  
Met His

1

ttc atg cag gag cac acc tgc tac gat gcc atg gcg acc agc tcc aaa 525  
Phe Met Gln Glu His Thr Cys Tyr Asp Ala Met Ala Thr Ser Ser Lys

5

10

15

2/20

ctg gtc atc ttc gac acc atg ctg gag atc aag aag gcc ttc ttt gcc	573
Leu Val Ile Phe Asp Thr Met Leu Glu Ile Lys Lys Ala Phe Phe Ala	
20 25 30	
ctg gtg gcc aac ggc gtc cga gcg gca cct ttg tgg gac agc aag aag	621
Leu Val Ala Asn Gly Val Arg Ala Ala Pro Leu Trp Asp Ser Lys Lys	
35 40 45 50	
cag agc ttc gtg ggg atg ctg acc atc aca gac ttc atc ttg gtg ctg	669
Gln Ser Phe Val Gly Met Leu Thr Ile Thr Asp Phe Ile Leu Val Leu	
55 60 65	
cac cgc tat tac agg tcc ccc ctg gtc cag atc tac gag att gaa gaa	717
His Arg Tyr Tyr Arg Ser Pro Leu Val Gln Ile Tyr Glu Ile Glu Glu	
70 75 80	
cat aag att gag acc tgg agg gag atc tac ctt caa ggc tgc ttc aag	765
His Lys Ile Glu Thr Trp Arg Glu Ile Tyr Leu Gln Gly Cys Phe Lys	
85 90 95	
cct ctg gtc tcc atc tct ccc aat gac agc ctg ttc gaa gct gtc tac	813
Pro Leu Val Ser Ile Ser Pro Asn Asp Ser Leu Phe Glu Ala Val Tyr	
100 105 110	
gcc ctc atc aag aac cgg atc cac cgc ctg ccg gtc ctg gac cct gtc	861
Ala Leu Ile Lys Asn Arg Ile His Arg Leu Pro Val Leu Asp Pro Val	
115 120 125 130	
tcc ggg gct gtg ctc cac atc ctc aca cat aag cgg ctt ctc aag ttc	909
Ser Gly Ala Val Leu His Ile Leu Thr His Lys Arg Leu Leu Lys Phe	
135 140 145	
ctg cac atc ttt ggc acc ctg ctg ccc cgg ccc tcc ttc ctc tac cgc	957
Leu His Ile Phe Gly Thr Leu Leu Pro Arg Pro Ser Phe Leu Tyr Arg	
150 155 160	
acc atc caa gat ttg ggc atc ggc aca ttc cga gac ttg gcc gtg gtg	1005
Thr Ile Gln Asp Leu Gly Ile Gly Thr Phe Arg Asp Leu Ala Val Val	
165 170 175	
ctg gaa acg gcg ccc atc ctg acc gca ctg gac atc ttc gtg gac cgg	1053
Leu Glu Thr Ala Pro Ile Leu Thr Ala Leu Asp Ile Phe Val Asp Arg	
180 185 190	
cgt gtg tct gcg ctg cct gtg gtc aac gaa act gga cag gta gtg ggc	1101
Arg Val Ser Ala Leu Pro Val Val Asn Glu Thr Gly Gln Val Val Gly	
195 200 205 210	
ctc tac tct cgc ttt gat gtg atc cac ctg gct gcc caa caa aca tac	1149
Leu Tyr Ser Arg Phe Asp Val Ile His Leu Ala Ala Gln Gln Thr Tyr	
215 220 225	
aac cac ctg gac atg aat gtg gga gaa gcc ctg agg cag cgg aca ctg	1197
Asn His Leu Asp Met Asn Val Gly Glu Ala Leu Arg Gln Arg Thr Leu	
230 235 240	
tgt ctg gaa ggc gtc ctt tcc tgc cag ccc cac gag acc ttg ggg gaa	1245
Cys Leu Glu Gly Val Leu Ser Cys Gln Pro His Glu Thr Leu Gly Glu	
245 250 255	

3/20

gtc att gac cgg att gtc cgg gaa cag gtg cac cgc ctg gtg ctc gtg 1293  
 Val Ile Asp Arg Ile Val Arg Glu Gln Val His Arg Leu Val Leu Val  
 260 265 270

gat gag acc cag cac ctt ctg ggc gtg gtg tcc ctc tct gac atc ctt 1341  
 Asp Glu Thr Gln His Leu Leu Gly Val Val Ser Leu Ser Asp Ile Leu  
 275 280 285 290

cag gct ctg gtg ctc agc cct gct gga att gat gcc ctc ggg gcc tga 1389  
 Gln Ala Leu Val Leu Ser Pro Ala Gly Ile Asp Ala Leu Gly Ala  
 295 300 305

gaaccttgga acctttgctc tcaggccacc tggcacacct ggaagccagt gaagggagcc 1449

gtggactcag ctctcacttc cctcagccc cacttgctgg tctggctctt gttcaggtag 1509

gctccgcccg gggcccctgg cctcagcatc agcccctcag tctccctggg caccagatc 1569

tcagactggg gcacctgaa gatgggagtg gccagctta tagctgagca gccttggtgaa 1629

atctaccagc atcaagactc actgtgggac cactgctttg tcccattctc agctgaaatg 1689

atggagggcc tcataagagg ggtggacagg gcctggagta gaggccagat cagtgcgtg 1749

ccttcaggac ctccggggag ttagagctgc cctctctcag ttcagttccc cctgctgag 1809

aatgtccctg gaaggaagcc agttaataaa ccttggttgg atggaatttc cacactcg 1867

<210> 2

<211> 305

<212> PRT

<213> Sus scrofa

<400> 2

Met His Phe Met Gln Glu His Thr Cys Tyr Asp Ala Met Ala Thr Ser  
 1 5 10 15

Ser Lys Leu Val Ile Phe Asp Thr Met Leu Glu Ile Lys Lys Ala Phe  
 20 25 30

Phe Ala Leu Val Ala Asn Gly Val Arg Ala Ala Pro Leu Trp Asp Ser  
 35 40 45

Lys Lys Gln Ser Phe Val Gly Met Leu Thr Ile Thr Asp Phe Ile Leu  
 50 55 60

Val Leu His Arg Tyr Tyr Arg Ser Pro Leu Val Gln Ile Tyr Glu Ile  
 65 70 75 80

Glu Glu His Lys Ile Glu Thr Trp Arg Glu Ile Tyr Leu Gln Gly Cys  
 85 90 95

Phe Lys Pro Leu Val Ser Ile Ser Pro Asn Asp Ser Leu Phe Glu Ala  
 100 105 110

Val Tyr Ala Leu Ile Lys Asn Arg Ile His Arg Leu Pro Val Leu Asp  
 115 120 125

Pro Val Ser Gly Ala Val Leu His Ile Leu Thr His Lys Arg Leu Leu  
 130 135 140

4/20

Lys Phe Leu His Ile Phe Gly Thr Leu Leu Pro Arg Pro Ser Phe Leu  
 145 150 155 160  
 Tyr Arg Thr Ile Gln Asp Leu Gly Ile Gly Thr Phe Arg Asp Leu Ala  
 165 170 175  
 Val Val Leu Glu Thr Ala Pro Ile Leu Thr Ala Leu Asp Ile Phe Val  
 180 185 190  
 Asp Arg Arg Val Ser Ala Leu Pro Val Val Asn Glu Thr Gly Gln Val  
 195 200 205  
 Val Gly Leu Tyr Ser Arg Phe Asp Val Ile His Leu Ala Ala Gln Gln  
 210 215 220  
 Thr Tyr Asn His Leu Asp Met Asn Val Gly Glu Ala Leu Arg Gln Arg  
 225 230 235 240  
 Thr Leu Cys Leu Glu Gly Val Leu Ser Cys Gln Pro His Glu Thr Leu  
 245 250 255  
 Gly Glu Val Ile Asp Arg Ile Val Arg Glu Gln Val His Arg Leu Val  
 260 265 270  
 Leu Val Asp Glu Thr Gln His Leu Leu Gly Val Val Ser Leu Ser Asp  
 275 280 285  
 Ile Leu Gln Ala Leu Val Leu Ser Pro Ala Gly Ile Asp Ala Leu Gly  
 290 295 300  
 Ala  
 305

<210> 3  
 <211> 2109  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (472) .. (1389)

<400> 3  
 ttcttagagc aagaaaacag cagctcatgg ccataccag ctgtgaccag cagctcagaa 60  
 agaatccgtg ggaaacggag ggccaaagcc ttgagatgga caaggcagaa gtcggtggag 120  
 gaaggggagc caccaggtca gggggaaggt ccccggtcca ggccaactgc tgagtccacc 180  
 gggctggagg ccacattccc caagaccaca cccttggtc aagctgatcc tgccgggggtg 240  
 ggcactccac caacaggggtg ggactgcctc ccctctgact gtacagcctc agctgcaggc 300  
 tccagcacag atgatgtgga gctggccacg gagttcccag ccacagaggc ctgggagtg 360  
 gagctagaag gcctgctgga agagaggcct gccctgtgcc tgtccccgca ggccccattt 420  
 cccaagctgg gctgggatga cgaactgcgg aaaccggcg cccagatcta c atg cgc 477

5/20

Met Arg  
1

ttc atg cag gag cac acc tgc tac gat gcc atg gca act agc tcc aag	525
Phe Met Gln Glu His Thr Cys Tyr Asp Ala Met Ala Thr Ser Ser Lys	
5 10 15	
cta gtc atc ttc gac acc atg ctg gag atc aag aag gcc ttc ttt gct	573
Leu Val Ile Phe Asp Thr Met Leu Glu Ile Lys Lys Ala Phe Phe Ala	
20 25 30	
ctg gtg gcc aac ggt gtg cgg gca gcc cct cta tgg gac agc aag aag	621
Leu Val Ala Asn Gly Val Arg Ala Ala Pro Leu Trp Asp Ser Lys Lys	
35 40 45 50	
cag agc ttt gtg ggg atg ctg acc atc act gac ttc atc ctg gtg ctg	669
Gln Ser Phe Val Gly Met Leu Thr Ile Thr Asp Phe Ile Leu Val Leu	
55 60 65	
cat cgc tac tac agg tcc ccc ctg gtc cag atc tat gag att gaa caa	717
His Arg Tyr Tyr Arg Ser Pro Leu Val Gln Ile Tyr Glu Ile Glu Gln	
70 75 80	
cat aag att gag acc tgg agg gag atc tac ctg caa ggc tgc ttc aag	765
His Lys Ile Glu Thr Trp Arg Glu Ile Tyr Leu Gln Gly Cys Phe Lys	
85 90 95	
cct ctg gtc tcc atc tct cct aat gat agc ctg ttt gaa gct gtc tac	813
Pro Leu Val Ser Ile Ser Pro Asn Asp Ser Leu Phe Glu Ala Val Tyr	
100 105 110	
acc ctc atc aag aac cgg atc cat cgc ctg cct gtt ctt gac ccg gtg	861
Thr Leu Ile Lys Asn Arg Ile His Arg Leu Pro Val Leu Asp Pro Val	
115 120 125 130	
tca ggc aac gta ctc cac atc ctc aca cac aaa cgc ctg ctc aag ttc	909
Ser Gly Asn Val Leu His Ile Leu Thr His Lys Arg Leu Leu Lys Phe	
135 140 145	
ctg cac atc ttt ggt tcc ctg ctg ccc cgg ccc tcc ttc ctc tac cgc	957
Leu His Ile Phe Gly Ser Leu Leu Pro Arg Pro Ser Phe Leu Tyr Arg	
150 155 160	
act atc caa gat ttg ggc atc ggc aca ttc cga gac ttg gct gtg gtg	1005
Thr Ile Gln Asp Leu Gly Ile Gly Thr Phe Arg Asp Leu Ala Val Val	
165 170 175	
ctg gag aca gca ccc atc ctg act gca ctg gac atc ttt gtg gac cgg	1053
Leu Glu Thr Ala Pro Ile Leu Thr Ala Leu Asp Ile Phe Val Asp Arg	
180 185 190	
cgt gtg tct gca ctg cct gtg gtc aac gaa tgt ggt cag gtc gtg ggc	1101
Arg Val Ser Ala Leu Pro Val Val Asn Glu Cys Gly Gln Val Val Gly	
195 200 205 210	
ctc tat tcc cgc ttt gat gtg att cac ctg gct gcc cag caa acc tac	1149
Leu Tyr Ser Arg Phe Asp Val Ile His Leu Ala Ala Gln Gln Thr Tyr	
215 220 225	

6/20

aac cac ctg gac atg agt gtg gga gaa gcc ctg agg cag agg aca cta 1197  
 Asn His Leu Asp Met Ser Val Gly Glu Ala Leu Arg Gln Arg Thr Leu  
                   230                                  235                                  240

tgt ctg gag gga gtc ctt tcc tgc cag ccc cac gag agc ttg ggg gaa 1245  
 Cys Leu Glu Gly Val Leu Ser Cys Gln Pro His Glu Ser Leu Gly Glu  
                   245                                  250                                  255

gtg atc gac agg att gct cgg gag cag gta cac agg ctg gtg cta gtg 1293  
 Val Ile Asp Arg Ile Ala Arg Glu Gln Val His Arg Leu Val Leu Val  
                   260                                  265                                  270

gac gag acc cag cat ctc ttg ggc gtg gtc tcc ctc tcc gac atc ctt 1341  
 Asp Glu Thr Gln His Leu Leu Gly Val Val Ser Leu Ser Asp Ile Leu  
                   275                                  280                                  285                                  290

cag gca ctg gtg ctc agc cct gct ggc atc gat gcc ctc ggg gcc tga 1389  
 Gln Ala Leu Val Leu Ser Pro Ala Gly Ile Asp Ala Leu Gly Ala  
                                   295                                  300                                  305

gaagatctga gtcctcaatc ccaagccaac tgcacactgg aagccaatga aggaattgag 1449

aacagcttca tttccccaac cccaatttgc tgggttcagct atgattcagg cttcttcagc 1509

cttccaaaat tgcctttgcc ttacttgtgc tcccagaacc cttcgggcat gcccagtgca 1569

ccatgggatg atgaaattaa ggagaacagc tgagtcaagc ttggaggtcc ctgaaccaga 1629

ggcactagga ttaccccagg gccatctgtg ctccatgccc gcccatcccc ttgccgcctg 1689

actgggtcgg atggccccag tgggtttagt cagggcttct ggattcctcg gtttctgggc 1749

tacctatggc ttcagccttc agctcctggg agtcccagct gttgttccca gcaacgtcgc 1809

cactgccctc ctactctcca ggctttgtca tttcaaggct gctgaaatgc tgcatttcag 1869

gggccaccat ggagcagccg ttatttatag aactgcctgt tggaggtggg gagtctccc 1929

tccattcttg tccagaaaac tccttagctc tcgcagttag ccatgttctt agtctccagg 1989

gatggatggc cttgtatatg gacccttag aatgagcaat tgagaaaaca aaacaaaagg 2049

aacaatccat gaacttagat tttattgggt tcaactcaaaa tgctgcagtc atttgacctg 2109

<210> 4

<211> 305

<212> PRT

<213> Homo sapiens

<400> 4

Met Arg Phe Met Gln Glu His Thr Cys Tyr Asp Ala Met Ala Thr Ser  
           1                                  5                                  10                                  15

Ser Lys Leu Val Ile Phe Asp Thr Met Leu Glu Ile Lys Lys Ala Phe  
                   20                                  25                                  30

Phe Ala Leu Val Ala Asn Gly Val Arg Ala Ala Pro Leu Trp Asp Ser  
           35                                  40                                  45

7/20

Lys Lys Gln Ser Phe Val Gly Met Leu Thr Ile Thr Asp Phe Ile Leu  
     50                    55                    60  
 Val Leu His Arg Tyr Tyr Arg Ser Pro Leu Val Gln Ile Tyr Glu Ile  
     65                    70                    75                    80  
 Glu Gln His Lys Ile Glu Thr Trp Arg Glu Ile Tyr Leu Gln Gly Cys  
                     85                    90                    95  
 Phe Lys Pro Leu Val Ser Ile Ser Pro Asn Asp Ser Leu Phe Glu Ala  
                     100                    105                    110  
 Val Tyr Thr Leu Ile Lys Asn Arg Ile His Arg Leu Pro Val Leu Asp  
                     115                    120                    125  
 Pro Val Ser Gly Asn Val Leu His Ile Leu Thr His Lys Arg Leu Leu  
                     130                    135                    140  
 Lys Phe Leu His Ile Phe Gly Ser Leu Leu Pro Arg Pro Ser Phe Leu  
     145                    150                    155                    160  
 Tyr Arg Thr Ile Gln Asp Leu Gly Ile Gly Thr Phe Arg Asp Leu Ala  
                     165                    170                    175  
 Val Val Leu Glu Thr Ala Pro Ile Leu Thr Ala Leu Asp Ile Phe Val  
                     180                    185                    190  
 Asp Arg Arg Val Ser Ala Leu Pro Val Val Asn Glu Cys Gly Gln Val  
                     195                    200                    205  
 Val Gly Leu Tyr Ser Arg Phe Asp Val Ile His Leu Ala Ala Gln Gln  
     210                    215                    220  
 Thr Tyr Asn His Leu Asp Met Ser Val Gly Glu Ala Leu Arg Gln Arg  
     225                    230                    235                    240  
 Thr Leu Cys Leu Glu Gly Val Leu Ser Cys Gln Pro His Glu Ser Leu  
                     245                    250                    255  
 Gly Glu Val Ile Asp Arg Ile Ala Arg Glu Gln Val His Arg Leu Val  
                     260                    265                    270  
 Leu Val Asp Glu Thr Gln His Leu Leu Gly Val Val Ser Leu Ser Asp  
                     275                    280                    285  
 Ile Leu Gln Ala Leu Val Leu Ser Pro Ala Gly Ile Asp Ala Leu Gly  
     290                    295                    300  
 Ala  
 305

<210> 5  
 <211> 20  
 <212> DNA  
 <213> Sus scrofa

<400> 5  
 ggaatttcaa gtcagccaac

8/20

<210> 6  
<211> 20  
<212> DNA  
<213> Sus scrofa

<400> 6  
cttcaaaaga ccgtgctact 20

<210> 7  
<211> 20  
<212> DNA  
<213> Sus scrofa

<400> 7  
ctgggaacct ctatatgctg 20

<210> 8  
<211> 20  
<212> DNA  
<213> Sus scrofa

<400> 8  
tagggaaata caaatcacag 20

<210> 9  
<211> 20  
<212> DNA  
<213> Sus scrofa

<400> 9  
ctccagctca caggatgaca 20

<210> 10  
<211> 26  
<212> DNA  
<213> Sus scrofa

<400> 10  
gtttctgcag ctttagcatc tattcc 26

<210> 11  
<211> 20  
<212> DNA  
<213> Sus scrofa

<400> 11  
gaagtatcct gggcttctga 20

<210> 12  
<211> 26  
<212> DNA  
<213> Sus scrofa

<400> 12



9/20

gtttctccag gtttccagac atccac

26

<210> 13  
<211> 20  
<212> DNA  
<213> Sus scrofa

<400> 13  
gcttctgtct gcccctactt

20

<210> 14  
<211> 26  
<212> DNA  
<213> Sus scrofa

<400> 14  
gtttctaagt tctactgtaa gacacc

26

<210> 15  
<211> 20  
<212> DNA  
<213> Sus scrofa

<400> 15  
ccaagctgtg gtggctgaat

20

<210> 16  
<211> 20  
<212> DNA  
<213> Sus scrofa

<400> 16  
cagcacagca gtgccaccta

20

<210> 17  
<211> 19  
<212> DNA  
<213> Sus scrofa

<400> 17  
caaactcttc taggcgtgt

19

<210> 18  
<211> 26  
<212> DNA  
<213> Sus scrofa

<400> 18  
gtttctggaa cttccatatg ccatgg

26

<210> 19  
<211> 20  
<212> DNA  
<213> Sus scrofa

10/20

<400> 19  
aggggtggatg gtaggcttca

20

<210> 20  
<211> 20  
<212> DNA  
<213> Sus scrofa

<400> 20  
gtctcgctcc tgaaggaagt

20

<210> 21  
<211> 20  
<212> DNA  
<213> Sus scrofa

<400> 21  
agtcacgtgg ccatgctatc

20

<210> 22  
<211> 20  
<212> DNA  
<213> Sus scrofa

<400> 22  
ctcaactgga ttgagtcagt

20

<210> 23  
<211> 20  
<212> DNA  
<213> Sus scrofa

<400> 23  
ttggcgcaac tgttatttct

20

<210> 24  
<211> 19  
<212> DNA  
<213> Sus scrofa

<400> 24  
aggcaaagga agagcacag

19

<210> 25  
<211> 18  
<212> DNA  
<213> Sus scrofa

<400> 25  
agccgtgggc atcgttgg

18

<210> 26  
<211> 21

11/20

&lt;212&gt; DNA

&lt;213&gt; Sus scrofa

&lt;400&gt; 26

agaaggagac agacagggcga

21

&lt;210&gt; 27

&lt;211&gt; 1873

&lt;212&gt; ADN

&lt;213&gt; Sus scrofa

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1) .. (1395)

&lt;400&gt; 27

atg agc ttc cta gag caa gga gag agc cgt tca tgg cca tcc cga gct	48
Met Ser Phe Leu Glu Gln Gly Glu Ser Arg Ser Trp Pro Ser Arg Ala	
1 5 10 15	
gta acc acc agc tca gaa aga agc cat ggg gac cag ggg aac aag gcc	96
Val Thr Thr Ser Ser Glu Arg Ser His Gly Asp Gln Gly Asn Lys Ala	
20 25 30	
tct aga tgg aca agg cag gag gat gta gag gaa ggg ggg cct ccg ggc	144
Ser Arg Trp Thr Arg Gln Glu Asp Val Glu Glu Gly Gly Pro Pro Gly	
35 40 45	
ccg agg gaa ggt ccc cag tcc agg cca gtt gct gag tcc acc ggg cag	192
Pro Arg Glu Gly Pro Gln Ser Arg Pro Val Ala Glu Ser Thr Gly Gln	
50 55 60	
gag gcc aca ttc ccc aag gcc aca ccc ttg gcc caa gcc gct ccc ttg	240
Glu Ala Thr Phe Pro Lys Ala Thr Pro Leu Ala Gln Ala Ala Pro Leu	
65 70 75 80	
gcc gag gtg gac aac ccc cca aca gag cgg gac atc ctc ccc tct gac	288
Ala Glu Val Asp Asn Pro Pro Thr Glu Arg Asp Ile Leu Pro Ser Asp	
85 90 95	
tgt gca gcc tca gcc tcc gac tcc aac aca gac cat ctg gat ctg ggc	336
Cys Ala Ala Ser Ala Ser Asp Ser Asn Thr Asp His Leu Asp Leu Gly	
100 105 110	
ata gag ttc tca gcc tcg gcg gcg tcg ggg gat gag ctt ggg ctg gtg	384
Ile Glu Phe Ser Ala Ser Ala Ala Ser Gly Asp Glu Leu Gly Leu Val	
115 120 125	
gaa gag aag cca gcc ccg tgc cca tcc cca gag gtg ctg tta ccc agg	432
Glu Glu Lys Pro Ala Pro Cys Pro Ser Pro Glu Val Leu Leu Pro Arg	
130 135 140	
ctg ggc tgg gat gat gag ctg cag aag ccg ggg gcc cag gtc tac atg	480
Leu Gly Trp Asp Asp Glu Leu Gln Lys Pro Gly Ala Gln Val Tyr Met	
145 150 155 160	
cac ttc atg cag gag cac acc tgc tac gat gcc atg gcg acc agc tcc	528
His Phe Met Gln Glu His Thr Cys Tyr Asp Ala Met Ala Thr Ser Ser	
165 170 175	

12/20

aaa ctg gtc atc ttc gac acc atg ctg gag atc aag aag gcc ttc ttt	576
Lys Leu Val Ile Phe Asp Thr Met Leu Glu Ile Lys Lys Ala Phe Phe	
180 185 190	
gcc ctg gtg gcc aac ggc gtc cga gcg gca cct ttg tgg gac agc aag	624
Ala Leu Val Ala Asn Gly Val Arg Ala Ala Pro Leu Trp Asp Ser Lys	
195 200 205	
aag cag agc ttc gtg ggg atg ctg acc atc aca gac ttc atc ttg gtg	672
Lys Gln Ser Phe Val Gly Met Leu Thr Ile Thr Asp Phe Ile Leu Val	
210 215 220	
ctg cac cgc tat tac agg tcc ccc ctg gtc cag atc tac gag att gaa	720
Leu His Arg Tyr Tyr Arg Ser Pro Leu Val Gln Ile Tyr Glu Ile Glu	
225 230 235 240	
gaa cat aag att gag acc tgg agg gag atc tac ctt caa ggc tgc ttc	768
Glu His Lys Ile Glu Thr Trp Arg Glu Ile Tyr Leu Gln Gly Cys Phe	
245 250 255	
aag cct ctg gtc tcc atc tct ccc aat gac agc ctg ttc gaa gct gtc	816
Lys Pro Leu Val Ser Ile Ser Pro Asn Asp Ser Leu Phe Glu Ala Val	
260 265 270	
tac gcc ctc atc aag aac cgg atc cac cgc ctg ccg gtc ctg gac cct	864
Tyr Ala Leu Ile Lys Asn Arg Ile His Arg Leu Pro Val Leu Asp Pro	
275 280 285	
gtc tcc ggg gct gtg ctc cac atc ctc aca cat aag cgg ctt ctc aag	912
Val Ser Gly Ala Val Leu His Ile Leu Thr His Lys Arg Leu Leu Lys	
290 295 300	
ttc ctg cac atc ttt ggc acc ctg ctg ccc cgg ccc tcc ttc ctc tac	960
Phe Leu His Ile Phe Gly Thr Leu Leu Pro Arg Pro Ser Phe Leu Tyr	
305 310 315 320	
cgc acc atc caa gat ttg ggc atc ggc aca ttc cga gac ttg gcc gtg	1008
Arg Thr Ile Gln Asp Leu Gly Ile Gly Thr Phe Arg Asp Leu Ala Val	
325 330 335	
gtg ctg gaa acg gcg ccc atc ctg acc gca ctg gac atc ttc gtg gac	1056
Val Leu Glu Thr Ala Pro Ile Leu Thr Ala Leu Asp Ile Phe Val Asp	
340 345 350	
cgg cgt gtg tct gcg ctg cct gtg gtc aac gaa act gga cag gta gtg	1104
Arg Arg Val Ser Ala Leu Pro Val Val Asn Glu Thr Gly Gln Val Val	
355 360 365	
ggc ctc tac tct cgc ttt gat gtg atc cac ctg gct gcc caa caa aca	1152
Gly Leu Tyr Ser Arg Phe Asp Val Ile His Leu Ala Ala Gln Gln Thr	
370 375 380	
tac aac cac ctg gac atg aat gtg gga gaa gcc ctg agg cag cgg aca	1200
Tyr Asn His Leu Asp Met Asn Val Gly Glu Ala Leu Arg Gln Arg Thr	
385 390 395 400	
ctg tgt ctg gaa ggc gtc ctt tcc tgc cag ccc cac gag acc ttg ggg	1248
Leu Cys Leu Glu Gly Val Leu Ser Cys Gln Pro His Glu Thr Leu Gly	
405 410 415	

13/20

gaa gtc att gac cgg att gtc cgg gaa cag gtg cac cgc ctg gtg ctc 1296  
 Glu Val Ile Asp Arg Ile Val Arg Glu Gln Val His Arg Leu Val Leu  
                   420                  425                  430

gtg gat gag acc cag cac ctt ctg ggc gtg gtg tcc ctc tct gac atc 1344  
 Val Asp Glu Thr Gln His Leu Leu Gly Val Val Ser Leu Ser Asp Ile  
                   435                  440                  445

ctt cag gct ctg gtg ctc agc cct gct gga att gat gcc ctc ggg gcc 1392  
 Leu Gln Ala Leu Val Leu Ser Pro Ala Gly Ile Asp Ala Leu Gly Ala  
                   450                  455                  460

tga gaaccttgga acctttgctc tcaggccacc tggcacacct ggaagccagt 1445  
 465

gaagggagcc gtggactcag ctctcacttc ccctcagccc cacttgctgg tctggtctctt 1505  
 gttcaggtag gctccgcccc gggcccttg cctcagcatc agcccctcag tctccctggg 1565  
 caccagatc tcagactggg gcaccctgaa gatgggagtg gccagctta tagctgagca 1625  
 gccttgtaaa atctaccagc atcaagactc actgtgggac cactgctttg tcccattctc 1685  
 agctgaaatg atggagggcc tcataagagg ggtggacagg gcctggagta gaggccagat 1745  
 cagtgaagtg ccttcaggac ctccggggag ttagagctgc cctctctcag ttcagttccc 1805  
 ccctgctgag aatgtccctg gaaggaagcc agttaataaa ccttggttgg atggaatttg 1865  
 gagagtcg 1873

<210> 28  
 <211> 464  
 <212> PRT  
 <213> Sus scrofa

<400> 28  
 Met Ser Phe Leu Glu Gln Gly Glu Ser Arg Ser Trp Pro Ser Arg Ala  
   1                  5                  10                  15  
 Val Thr Thr Ser Ser Glu Arg Ser His Gly Asp Gln Gly Asn Lys Ala  
                   20                  25                  30  
 Ser Arg Trp Thr Arg Gln Glu Asp Val Glu Glu Gly Gly Pro Pro Gly  
                   35                  40                  45  
 Pro Arg Glu Gly Pro Gln Ser Arg Pro Val Ala Glu Ser Thr Gly Gln  
                   50                  55                  60  
 Glu Ala Thr Phe Pro Lys Ala Thr Pro Leu Ala Gln Ala Ala Pro Leu  
                   65                  70                  75                  80  
 Ala Glu Val Asp Asn Pro Pro Thr Glu Arg Asp Ile Leu Pro Ser Asp  
                   85                  90                  95  
 Cys Ala Ala Ser Ala Ser Asp Ser Asn Thr Asp His Leu Asp Leu Gly  
                   100                  105                  110  
 Ile Glu Phe Ser Ala Ser Ala Ala Ser Gly Asp Glu Leu Gly Leu Val  
                   115                  120                  125  
 Glu Glu Lys Pro Ala Pro Cys Pro Ser Pro Glu Val Leu Leu Pro Arg  
                   130                  135                  140  
 Leu Gly Trp Asp Asp Glu Leu Gln Lys Pro Gly Ala Gln Val Tyr Met  
                   145                  150                  155                  160  
 His Phe Met Gln Glu His Thr Cys Tyr Asp Ala Met Ala Thr Ser Ser  
                   165                  170                  175

14/20

Lys Leu Val Ile Phe Asp Thr Met Leu Glu Ile Lys Lys Ala Phe Phe  
 180 185 190  
 Ala Leu Val Ala Asn Gly Val Arg Ala Ala Pro Leu Trp Asp Ser Lys  
 195 200 205  
 Lys Gln Ser Phe Val Gly Met Leu Thr Ile Thr Asp Phe Ile Leu Val  
 210 215 220  
 Leu His Arg Tyr Tyr Arg Ser Pro Leu Val Gln Ile Tyr Glu Ile Glu  
 225 230 235 240  
 Glu His Lys Ile Glu Thr Trp Arg Glu Ile Tyr Leu Gln Gly Cys Phe  
 245 250 255  
 Lys Pro Leu Val Ser Ile Ser Pro Asn Asp Ser Leu Phe Glu Ala Val  
 260 265 270  
 Tyr Ala Leu Ile Lys Asn Arg Ile His Arg Leu Pro Val Leu Asp Pro  
 275 280 285  
 Val Ser Gly Ala Val Leu His Ile Leu Thr His Lys Arg Leu Leu Lys  
 290 295 300  
 Phe Leu His Ile Phe Gly Thr Leu Leu Pro Arg Pro Ser Phe Leu Tyr  
 305 310 315 320  
 Arg Thr Ile Gln Asp Leu Gly Ile Gly Thr Phe Arg Asp Leu Ala Val  
 325 330 335  
 Val Leu Glu Thr Ala Pro Ile Leu Thr Ala Leu Asp Ile Phe Val Asp  
 340 345 350  
 Arg Arg Val Ser Ala Leu Pro Val Val Asn Glu Thr Gly Gln Val Val  
 355 360 365  
 Gly Leu Tyr Ser Arg Phe Asp Val Ile His Leu Ala Ala Gln Gln Thr  
 370 375 380  
 Tyr Asn His Leu Asp Met Asn Val Gly Glu Ala Leu Arg Gln Arg Thr  
 385 390 395 400  
 Leu Cys Leu Glu Gly Val Leu Ser Cys Gln Pro His Glu Thr Leu Gly  
 405 410 415  
 Glu Val Ile Asp Arg Ile Val Arg Glu Gln Val His Arg Leu Val Leu  
 420 425 430  
 Val Asp Glu Thr Gln His Leu Leu Gly Val Val Ser Leu Ser Asp Ile  
 435 440 445  
 Leu Gln Ala Leu Val Leu Ser Pro Ala Gly Ile Asp Ala Leu Gly Ala  
 450 455 460

<210> 29  
 <211> 2115  
 <212> ADN  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (1)..(1395)

<400> 29  
 atg agc ttc cta gag caa gaa aac agc agc tca tgg cca tca cca gct 48  
 Met Ser Phe Leu Glu Gln Glu Asn Ser Ser Ser Trp Pro Ser Pro Ala  
 1 5 10 15  
 gtg acc agc agc tca gaa aga atc cgt ggg aaa cgg agg gcc aaa gcc 96  
 Val Thr Ser Ser Ser Glu Arg Ile Arg Gly Lys Arg Arg Ala Lys Ala  
 20 25 30  
 ttg aga tgg aca agg cag aag tcg gtg gag gaa ggg gag cca cca ggt 144  
 Leu Arg Trp Thr Arg Gln Lys Ser Val Glu Glu Gly Glu Pro Pro Gly  
 35 40 45

15/20

cag ggg gaa ggt ccc cgg tcc agg cca act gct gag tcc acc ggg ctg	192
Gln Gly Glu Gly Pro Arg Ser Arg Pro Thr Ala Glu Ser Thr Gly Leu	
50 55 60	
 gag gcc aca ttc ccc aag acc aca ccc ttg gct caa gct gat cct gcc	240
Glu Ala Thr Phe Pro Lys Thr Thr Pro Leu Ala Gln Ala Asp Pro Ala	
65 70 75 80	
 ggg gtg ggc act cca cca aca ggg tgg gac tgc ctc ccc tct gac tgt	288
Gly Val Gly Thr Pro Pro Thr Gly Trp Asp Cys Leu Pro Ser Asp Cys	
85 90 95	
 aca gcc tca gct gca ggc tcc agc aca gat gat gtg gag ctg gcc acg	336
Thr Ala Ser Ala Ala Gly Ser Ser Thr Asp Asp Val Glu Leu Ala Thr	
100 105 110	
 gag ttc cca gcc aca gag gcc tgg gag tgt gag cta gaa ggc ctg ctg	384
Glu Phe Pro Ala Thr Glu Ala Trp Glu Cys Glu Leu Glu Gly Leu Leu	
115 120 125	
 gaa gag agg cct gcc ctg tgc ctg tcc ccg cag gcc cca ttt ccc aag	432
Glu Glu Arg Pro Ala Leu Cys Leu Ser Pro Gln Ala Pro Phe Pro Lys	
130 135 140	
 ctg ggc tgg gat gac gaa ctg cgg aaa ccc ggc gcc cag atc tac atg	480
Leu Gly Trp Asp Asp Glu Leu Arg Lys Pro Gly Ala Gln Ile Tyr Met	
145 150 155 160	
 cgc ttc atg cag gag cac acc tgc tac gat gcc atg gca act agc tcc	528
Arg Phe Met Gln Glu His Thr Cys Tyr Asp Ala Met Ala Thr Ser Ser	
165 170 175	
 aag cta gtc atc ttc gac acc atg ctg gag atc aag aag gcc ttc ttt	576
Lys Leu Val Ile Phe Asp Thr Met Leu Glu Ile Lys Lys Ala Phe Phe	
180 185 190	
 gct ctg gtg gcc aac ggt gtg cgg gca gcc cct cta tgg gac agc aag	624
Ala Leu Val Ala Asn Gly Val Arg Ala Ala Pro Leu Trp Asp Ser Lys	
195 200 205	
 aag cag agc ttt gtg ggg atg ctg acc atc act gac ttc atc ctg gtg	672
Lys Gln Ser Phe Val Gly Met Leu Thr Ile Thr Asp Phe Ile Leu Val	
210 215 220	
 ctg cat cgc tac tac agg tcc ccc ctg gtc cag atc tat gag att gaa	720
Leu His Arg Tyr Tyr Arg Ser Pro Leu Val Gln Ile Tyr Glu Ile Glu	
225 230 235 240	
 caa cat aag att gag acc tgg agg gag atc tac ctg caa ggc tgc ttc	768
Gln His Lys Ile Glu Thr Trp Arg Glu Ile Tyr Leu Gln Gly Cys Phe	
245 250 255	
 aag cct ctg gtc tcc atc tct cct aat gat agc ctg ttt gaa gct gtc	816
Lys Pro Leu Val Ser Ile Ser Pro Asn Asp Ser Leu Phe Glu Ala Val	
260 265 270	
 tac acc ctc atc aag aac cgg atc cat cgc ctg cct gtt ctt gac ccg	864
Tyr Thr Leu Ile Lys Asn Arg Ile His Arg Leu Pro Val Leu Asp Pro	
275 280 285	

16/20

gtg tca ggc aac gta ctc cac atc ctc aca cac aaa cgc ctg ctc aag 912  
 Val Ser Gly Asn Val Leu His Ile Leu Thr His Lys Arg Leu Leu Lys  
 290 295 300

ttc ctg cac atc ttt ggt tcc ctg ctg ccc cgg ccc tcc ttc ctc tac 960  
 Phe Leu His Ile Phe Gly Ser Leu Leu Pro Arg Pro Ser Phe Leu Tyr  
 305 310 315 320

cgc act atc caa gat ttg ggc atc ggc aca ttc cga gac ttg gct gtg 1008  
 Arg Thr Ile Gln Asp Leu Gly Ile Gly Thr Phe Arg Asp Leu Ala Val  
 325 330 335

gtg ctg gag aca gca ccc atc ctg act gca ctg gac atc ttt gtg gac 1056  
 Val Leu Glu Thr Ala Pro Ile Leu Thr Ala Leu Asp Ile Phe Val Asp  
 340 345 350

cgg cgt gtg tct gca ctg cct gtg gtc aac gaa tgt ggt cag gtc gtg 1104  
 Arg Arg Val Ser Ala Leu Pro Val Val Asn Glu Cys Gly Gln Val Val  
 355 360 365

ggc ctc tat tcc cgc ttt gat gtg att cac ctg gct gcc cag caa acc 1152  
 Gly Leu Tyr Ser Arg Phe Asp Val Ile His Leu Ala Ala Gln Gln Thr  
 370 375 380

tac aac cac ctg gac atg agt gtg gga gaa gcc ctg agg cag agg aca 1200  
 Tyr Asn His Leu Asp Met Ser Val Gly Glu Ala Leu Arg Gln Arg Thr  
 385 390 395 400

cta tgt ctg gag gga gtc ctt tcc tgc cag ccc cac gag agc ttg ggg 1248  
 Leu Cys Leu Glu Gly Val Leu Ser Cys Gln Pro His Glu Ser Leu Gly  
 405 410 415

gaa gtg atc gac agg att gct cgg gag cag gta cac agg ctg gtg cta 1296  
 Glu Val Ile Asp Arg Ile Ala Arg Glu Gln Val His Arg Leu Val Leu  
 420 425 430

gtg gac gag acc cag cat ctc ttg ggc gtg gtc tcc ctc tcc gac atc 1344  
 Val Asp Glu Thr Gln His Leu Leu Gly Val Val Ser Leu Ser Asp Ile  
 435 440 445

ctt cag gca ctg gtg ctc agc cct gct ggc atc gat gcc ctc ggg gcc 1392  
 Leu Gln Ala Leu Val Leu Ser Pro Ala Gly Ile Asp Ala Leu Gly Ala  
 450 455 460

tga gaagatctga gtcctcaatc ccaagccaac tgcacactgg aagccaatga 1445  
 465

aggaattgag aacagcttca tttccccaac cccaatttgc tggttcagct atgattcagg 1505

cttcttcagc cttccaaaat tgcctttgcc ttacttgtgc tcccagaacc cttcggggcat 1565

gccagtgca ccatgggatg atgaaattaa ggagaacagc tgagtcaagc ttggaggtcc 1625

ctgaaccaga ggcactagga ttaccccagg gccatctgtg ctccatgccc gcccatcccc 1685

ttgccgcctg actgggtcgg atggccccag tgggtttagt cagggcttct ggattcctcg 1745

gtttctgggc tacctatggc ttcagccttc agtctctggg agtcccagct gttgttccca 1805

gcaacgtcgc cactgccctc ctactetcca ggctttgtca tttcaaggct gctgaaatgc 1865



17/20

tgcatttcag gggccaccat ggagcagccg ttatttatag aactgcctgt tggaggtggg 1925  
 gagtcctccc tccattcttg tccagaaaac tccttagctc tcgcagtgag ccatgttctt 1985  
 agtctccagg gatggatggc cttgtatatg gacccttgag aatgagcaat tgagaaaaca 2045  
 aaacaaaagg aacaatccat gaacttagat tttattgggt tcaactcaaaa tgctgcagtc 2105  
 atttgacctg 2115

&lt;210&gt; 30

&lt;211&gt; 464

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 30

Met	Ser	Phe	Leu	Glu	Gln	Glu	Asn	Ser	Ser	Ser	Trp	Pro	Ser	Pro	Ala
1				5					10					15	
Val	Thr	Ser	Ser	Ser	Glu	Arg	Ile	Arg	Gly	Lys	Arg	Arg	Ala	Lys	Ala
			20					25					30		
Leu	Arg	Trp	Thr	Arg	Gln	Lys	Ser	Val	Glu	Glu	Gly	Glu	Pro	Pro	Gly
		35					40					45			
Gln	Gly	Glu	Gly	Pro	Arg	Ser	Arg	Pro	Thr	Ala	Glu	Ser	Thr	Gly	Leu
	50					55					60				
Glu	Ala	Thr	Phe	Pro	Lys	Thr	Thr	Pro	Leu	Ala	Gln	Ala	Asp	Pro	Ala
65					70					75				80	
Gly	Val	Gly	Thr	Pro	Pro	Thr	Gly	Trp	Asp	Cys	Leu	Pro	Ser	Asp	Cys
				85					90					95	
Thr	Ala	Ser	Ala	Ala	Gly	Ser	Ser	Thr	Asp	Asp	Val	Glu	Leu	Ala	Thr
			100					105					110		
Glu	Phe	Pro	Ala	Thr	Glu	Ala	Trp	Glu	Cys	Glu	Leu	Glu	Gly	Leu	Leu
	115						120					125			
Glu	Glu	Arg	Pro	Ala	Leu	Cys	Leu	Ser	Pro	Gln	Ala	Pro	Phe	Pro	Lys
	130					135					140				
Leu	Gly	Trp	Asp	Asp	Glu	Leu	Arg	Lys	Pro	Gly	Ala	Gln	Ile	Tyr	Met
145					150					155				160	
Arg	Phe	Met	Gln	Glu	His	Thr	Cys	Tyr	Asp	Ala	Met	Ala	Thr	Ser	Ser
			165						170					175	
Lys	Leu	Val	Ile	Phe	Asp	Thr	Met	Leu	Glu	Ile	Lys	Lys	Ala	Phe	Phe
		180						185						190	
Ala	Leu	Val	Ala	Asn	Gly	Val	Arg	Ala	Ala	Pro	Leu	Trp	Asp	Ser	Lys
	195						200					205			
Lys	Gln	Ser	Phe	Val	Gly	Met	Leu	Thr	Ile	Thr	Asp	Phe	Ile	Leu	Val
	210					215					220				
Leu	His	Arg	Tyr	Tyr	Arg	Ser	Pro	Leu	Val	Gln	Ile	Tyr	Glu	Ile	Glu
225					230					235				240	
Gln	His	Lys	Ile	Glu	Thr	Trp	Arg	Glu	Ile	Tyr	Leu	Gln	Gly	Cys	Phe
			245						250					255	
Lys	Pro	Leu	Val	Ser	Ile	Ser	Pro	Asn	Asp	Ser	Leu	Phe	Glu	Ala	Val
			260					265					270		
Tyr	Thr	Leu	Ile	Lys	Asn	Arg	Ile	His	Arg	Leu	Pro	Val	Leu	Asp	Pro
	275						280					285			
Val	Ser	Gly	Asn	Val	Leu	His	Ile	Leu	Thr	His	Lys	Arg	Leu	Leu	Lys
	290					295					300				
Phe	Leu	His	Ile	Phe	Gly	Ser	Leu	Leu	Pro	Arg	Pro	Ser	Phe	Leu	Tyr
305					310					315				320	
Arg	Thr	Ile	Gln	Asp	Leu	Gly	Ile	Gly	Thr	Phe	Arg	Asp	Leu	Ala	Val
			325						330					335	

18/20

Val Leu Glu Thr Ala Pro Ile Leu Thr Ala Leu Asp Ile Phe Val Asp  
 340 345 350  
 Arg Arg Val Ser Ala Leu Pro Val Asn Glu Cys Gly Gln Val Val  
 355 360 365  
 Gly Leu Tyr Ser Arg Phe Asp Val Ile His Leu Ala Ala Gln Gln Thr  
 370 375 380  
 Tyr Asn His Leu Asp Met Ser Val Gly Glu Ala Leu Arg Gln Arg Thr  
 385 390 395 400  
 Leu Cys Leu Glu Gly Val Leu Ser Cys Gln Pro His Glu Ser Leu Gly  
 405 410 415  
 Glu Val Ile Asp Arg Ile Ala Arg Glu Gln Val His Arg Leu Val Leu  
 420 425 430  
 Val Asp Glu Thr Gln His Leu Leu Gly Val Val Ser Leu Ser Asp Ile  
 435 440 445  
 Leu Gln Ala Leu Val Leu Ser Pro Ala Gly Ile Asp Ala Leu Gly Ala  
 450 455 460

<210> 31  
 <211> 2022  
 <212> ADN  
 <213> Sus scrofa

<400> 31  
 atggagcttg ccgagctaga gcaggcactg cgcagggtcc cgggggtccc ggggggctgg 60  
 gagctggagc aactgaggcc agagggcaga gggcccacca ctgcggatac tccctcctgg 120  
 agcagcctcg ggggacctaa gcatcaagag atgagcttcc tagagcaagg agagagccgt 180  
 tcatggccat cccgagctgt aaccaccagc tcagaaagaa gccatgggga ccagggggag 240  
 aaggcctcta gatggacaag gcaggaggat gtagaggaag gggggcctcc gggcccagg 300  
 gaaggtcccc agtccaggcc agttgctgag tccaccgggc aggaggccac attccccaag 360  
 gccacacctt tggcccaagc cgctcccttg gccgaggtgg acaaccccc aacagagcgg 420  
 gacatcctcc cctctgactg tgcagcctca gcctccgact ccaacacaga ccatctggat 480  
 ctgggcatag agttctcagc ctcggcggcg tcgggggatg agcttgggct ggtggaagag 540  
 aagccagccc cgtgcccata cccagaggtg ctgttaccca ggctgggctg ggatgatgag 600  
 ctgcagaagc cggggggcca ggtctacatg caattcatgc aggagcacac ctgctacgat 660  
 gccatggcga ccagctccaa actggtcatc ttcgacacca tgctggagat caagaaggcc 720  
 ttctttgccc tgggtggccaa cggcgctcca ggcgcacctt tgtgggacag caagaagcag 780  
 agcttcgtgg ggatgctgac catcacagac ttcatcttgg tgctgcaccg ctattacagg 840  
 tcccccttgg tccagatcta cgagattgaa gaacataaga ttgagacctg gagggagatc 900  
 taccttcaag gctgcttcaa gcctctggtc tccatctctc ccaatgacag cctgttcgaa 960  
 gctgtctacg cctcatcaa gaaccgcatc caccgcctgc cggctctgga ccctgtctcc 1020  
 ggggctgtgc tccacatcct cacacataag cggtctctca agttcctgca catcttggc 1080  
 accctgctgc cccggccctc ctctctctac cgcaccatcc aagatttggg catcggcaca 1140  
 ttccgagact tggccgtggg gctggaaaag gcgcccaccc tgaccgcact ggacatcttc 1200  
 gtggaccggc gtgtgtctgc gctgcctgtg gtcaacgaaa ctggacaggc agtgggcctc 1260  
 tactctcgtc ttgatgtgat ccacctggct gcccaacaaa catacaacca cctggacatg 1320  
 aatgtgggag aagccctgag gcagcggaca ctgtgtctgg aaggcgtcct ttcttgccag 1380  
 cccacagaga ccttggggga agtcattgac cggattgtcc gggaacaggc gcaccgcctg 1440  
 gtgctcgtgg atgagacca gcacctctg ggcgtgggtg cctctctga catccttcag 1500  
 gctctggtgc tcagccctgc tgggaattgat gccctcgggg cctgagaacc ttggaacctt 1560  
 tgctctcagg ccacctggca cacctggaag ccagtgaagg gagccgtgga ctacgtctc 1620  
 attccctc agccccactt gctgggtctg ctcttgttca ggtaggctcc gcccgggg 1680  
 cctggcctca gcacagccc ctacgtctcc ctgggcaccc agatctcaga ctggggcacc 1740  
 ctgaagatgg gactggccca gcttatagct gacagcctt gtgaaatcta ccagatcaa 1800  
 gactcactgt gggaccactg ctttgtccca ttctcagctg aaatgatgga gggcctcata 1860  
 agaggggtgg acagggcctg gagtagagc cagatcagtg acgtgccttc aggacctccg 1920  
 gggagttaga gctgcctctc ctacgttcag ttccccctg ctgagaatgt ccctggaagg 1980  
 aagccagtta ataaacctg gttggatgga atttggagag tc 2022

19/20

<210> 32  
 <211> 514  
 <212> PRT  
 <213> Sus scrofa

<400> 32

```

Met Glu Leu Ala Glu Leu Glu Gln Ala Leu Arg Arg Val Pro Gly Ser
  1           5           10           15

Arg Gly Gly Trp Glu Leu Glu Gln Leu Arg Pro Glu Gly Arg Gly Pro
      20           25           30

Thr Thr Ala Asp Thr Pro Ser Trp Ser Ser Leu Gly Gly Pro Lys His
      35           40           45

Gln Glu Met Ser Phe Leu Glu Gln Gly Glu Ser Arg Ser Trp Pro Ser
      50           55           60

Arg Ala Val Thr Thr Ser Ser Glu Arg Ser His Gly Asp Gln Gly Asn
      65           70           75           80

Lys Ala Ser Arg Trp Thr Arg Gln Glu Asp Val Glu Glu Gly Gly Pro
      85           90           95

Pro Gly Pro Arg Glu Gly Pro Gln Ser Arg Pro Val Ala Glu Ser Thr
      100          105          110

Gly Gln Glu Ala Thr Phe Pro Lys Ala Thr Pro Leu Ala Gln Ala Ala
      115          120          125

Pro Leu Ala Glu Val Asp Asn Pro Pro Thr Glu Arg Asp Ile Leu Pro
      130          135          140

Ser Asp Cys Ala Ala Ser Ala Ser Asp Ser Asn Thr Asp His Leu Asp
      145          150          155          160

Leu Gly Ile Glu Phe Ser Ala Ser Ala Ala Ser Gly Asp Glu Leu Gly
      165          170          175

Leu Val Glu Glu Lys Pro Ala Pro Cys Pro Ser Pro Glu Val Leu Leu
      180          185          190

Pro Arg Leu Gly Trp Asp Asp Glu Leu Gln Lys Pro Gly Ala Gln Val
      195          200          205

Tyr Met His Phe Met Gln Glu His Thr Cys Tyr Asp Ala Met Ala Thr
      210          215          220

Ser Ser Lys Leu Val Ile Phe Asp Thr Met Leu Glu Ile Lys Lys Ala
      225          230          235          240

Phe Phe Ala Leu Val Ala Asn Gly Val Arg Ala Ala Pro Leu Trp Asp
      245          250          255

Ser Lys Lys Gln Ser Phe Val Gly Met Leu Thr Ile Thr Asp Phe Ile
      260          265          270

Leu Val Leu His Arg Tyr Tyr Arg Ser Pro Leu Val Gln Ile Tyr Glu
      275          280          285

```

20/20

Ile Glu Glu His Lys Ile Glu Thr Trp Arg Glu Ile Tyr Leu Gln Gly  
 290 295 300  
 Cys Phe Lys Pro Leu Val Ser Ile Ser Pro Asn Asp Ser Leu Phe Glu  
 305 310 315 320  
 Ala Val Tyr Ala Leu Ile Lys Asn Arg Ile His Arg Leu Pro Val Leu  
 325 330 335  
 Asp Pro Val Ser Gly Ala Val Leu His Ile Leu Thr His Lys Arg Leu  
 340 345 350  
 Leu Lys Phe Leu His Ile Phe Gly Thr Leu Leu Pro Arg Pro Ser Phe  
 355 360 365  
 Leu Tyr Arg Thr Ile Gln Asp Leu Gly Ile Gly Thr Phe Arg Asp Leu  
 370 375 380  
 Ala Val Val Leu Glu Thr Ala Pro Ile Leu Thr Ala Leu Asp Ile Phe  
 385 390 395 400  
 Val Asp Arg Arg Val Ser Ala Leu Pro Val Val Asn Glu Thr Gly Gln  
 405 410 415  
 Val Val Gly Leu Tyr Ser Arg Phe Asp Val Ile His Leu Ala Ala Gln  
 420 425 430  
 Gln Thr Tyr Asn His Leu Asp Met Asn Val Gly Glu Ala Leu Arg Gln  
 435 440 445  
 Arg Thr Leu Cys Leu Glu Gly Val Leu Ser Cys Gln Pro His Glu Thr  
 450 455 460  
 Leu Gly Glu Val Ile Asp Arg Ile Val Arg Glu Gln Val His Arg Leu  
 465 470 475 480  
 Val Leu Val Asp Glu Thr Gln His Leu Leu Gly Val Val Ser Leu Ser  
 485 490 495  
 Asp Ile Leu Gln Ala Leu Val Leu Ser Pro Ala Gly Ile Asp Ala Leu  
 500 505 510  
 Gly Ala